

## **RESPONSE**

### **I. Status of the Claims**

Claims 1 and 4 were previously cancelled without prejudice or disclaimer. Claims 2, 3 and 8 are presently cancelled entirely without prejudice or disclaimer. Claims 5, 6 and 7 have been amended. Claim 9 has been added to better claim the present invention. As a result claims 5-7 and 9 are presently pending in this case.

### **II. Support for the Amended Claims**

Claim 5 has been revised to further clarify the claim and better claim the invention. Amended Claim 5 is fully supported by the specification, sequence listing and claims as originally filed with particular support being found in the specification at page 13 lines 18 -24, original Claim 3, previous Claim 5 and SEQ ID NO:1.

Claim 6 has been revised to further clarify the claim and better claim the invention. Amended Claim 6 is fully supported by the specification, sequence listing and claims as originally filed with particular support being found in the specification at page 13 lines 18 - 24, original claims 1-3, previous Claim 6 and SEQ ID NO:1.

Claim 7 has been revised to further clarify the claim and better claim the invention and to remove dependence on a cancelled claim. Amended Claim 7 is fully supported by the specification, sequence listing and claims as originally filed with particular support being found in the specification at page 13 lines 24 - 30, previous Claim 7 and SEQ ID NO:1.

New Claim 9 has been added to better and more clearly claim the present invention. Support for this claim can be found throughout the specification, sequence listing and claims as originally filed, with particular support being found in the specification at least at page 13, lines 28 through page 14 line 9.

As the revision of claims 5-7 and new Claim 9 are fully supported by the specification, the sequence listing and claims as originally filed, they do not constitute new matter. Entry therefore is respectfully requested.

### **III. Rejection of Claims Under 35 U.S.C. § 112, Second Paragraph**

The Action maintains the rejection of Claim 2 as allegedly indefinite based on the use of the phrase "highly stringent hybridization conditions" and because the specific hybridization and washing conditions are not recited in the claim. Applicants stress that "a claim need not 'describe' the invention, such description being the role of the disclosure". *Orthokinetics, Inc. v. Safety Travel Chairs, Inc.*, 1 USPQ2d 1081, 1088 (Fed. Cir. 1986). However, while Applicants in no way agree with this rejection, they note that as Claim 2 has been cancelled, this issue has been rendered moot and thus the rejection of Claim 2 under 35 U.S.C. § 112, second paragraph has been avoided. Applicants therefore respectfully request withdrawal of this rejection.

### **IV. Rejection of Claims Under 35 U.S.C. § 102(e)**

The Action maintains the rejection of the claims under 35 U.S.C. § 102(e), as allegedly anticipated by Spytek, *et al.* (WO 01/90155; "Spytek"). Applicants respectfully traverse.

Applicants attempted to remove Spytek as prior art with the submission of a properly executed Rule 131 declaration to evidence an invention date for the presently claimed invention in the United States prior to May 24, 2000, the effective filing date for the U.S. provisional application 60/206,688 in which Spytek first disclosed SEQ ID NOS: 3 and 4. However, as the Examiner has noted, "swearing behind" 102(e) art appears to be improper. Thus, in response Applicants have elected to amended the claims to read on SEQ ID NO: 1 and provide a sequence comparison between the nucleic acid sequence of SEQ ID NO:1 of the present invention and that of Spytek (**EXHIBIT A**). It is apparent from this comparison that these sequences are not identical. The sequence of Spytek has 5 additional nucleotides located at the 5 prime end and 10 additional nucleotides located at the 3 prime end of the sequence as compared to that of SEQ ID NO:1 of the present invention. Therefore, these sequences are not identical and rejection of the claims under 35 U.S.C. § 102(e), as allegedly anticipated by Spytek has been avoided and thus should be withdrawn.

### **V. Conclusion**

The present document is a full and complete response to the Action. In conclusion, Applicants submit that, in light of the foregoing remarks, the present case is in condition for allowance, and such

favorable action is respectfully requested. Should Examiner Prouty have any questions or comments, or believe that certain amendments of the claims might serve to improve their clarity, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Respectfully submitted,

September 24, 2004

Date

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Agent for Applicants

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FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaGAAB4ayCQ: 132 nt

>SEQ ID NO:1

vs /tmp/fastaHAAC4ayCQ library  
searching /tmp/fastaHAAC4ayCQ library

147 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, +5/-4 matrix (5:-4)] ktup: 6

join: 46, opt: 31, gap-pen: -16/ -4, width: 16

Scan time: 0.017

The best scores are:

opt

Spyteck et al.

( 147) [f] 660

Spyteck et al.

( 147) [r] 56

>>Spyteck et al.

(147 nt)

initn: 660 init1: 660 opt: 660

100.000% identity in 132 nt overlap (1-132:6-137)

```

              10          20          30          40          50
SEQ      ATGGCACACAACTAGACCTGGAAGAAATTGCCAGCTTGGATAAGGCCAAGCTGA
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Spytec  AGAAAATGGCACACAACTAGACCTGGAAGAAATTGCCAGCTTGGATAAGGCCAAGCTGA
              10          20          30          40          50          60

              60          70          80          90          100          110
SEQ      AGGCCACAGAGATGCAGAAGAACACTCTGATGACCAAAGAGACCACAGAGCAGGAGAAGT
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Spytec  AGGCCACAGAGATGCAGAAGAACACTCTGATGACCAAAGAGACCACAGAGCAGGAGAAGT
              70          80          90          100          110          120

              120          130
SEQ      GGAGTGAAATTCCTGA
          ::::::::::::::
Spytec  GGAGTGAAATTCCTGAGAGCCTCGAG
              130          140
```

>>Spyteck et al.

(147 nt)

rev-comp initn: 56 init1: 56 opt: 56

72.727% identity in 22 nt overlap (54-33:38-59)

```

              80          70          60          50          40          30
SEQ-     CAGAGTGTCTTCTGCATCTCTGTGGCCTTCAGCTTGGCCTTATCCAAGCTGGCAATTC
          ::::::::::::::::::::
Spytec  GGCACACAACTAGACCTGGAAGAAATTGCCAGCTTGGATAAGGCCAAGCTGAAGGCCAC
              10          20          30          40          50          60

              20          10
SEQ-     TTCCAGGTCTAGTTTGTGTGCCAT

Spytec  AGAGATGCAGAAGAACACTCTGATGACCAAAGAGACCACAGAGCAGGAGAAGTGGAGTGA
              70          80          90          100          110          120
```

132 residues in 1 query sequences

147 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Fri Sep 3 11:29:29 2004 done: Fri Sep 3 11:29:29 2004

Scan time: 0.017 Display time: 0.016

Function used was FASTA